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## UNCOVERING A DRAMATIC SHIFT IN MESSENGER RNA SECONDARY STRUCTURE DURING PLANT SALT STRESS RESPONSE

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At the heart of post-transcriptional regulatory pathways in Aceukaryotes are *cis*- and *trans*-acting features and factors including RNA secondary structure as well as RNA-Binding Proteins (RBPs) and their recognition sites on target RNAs. This is especially evident for RNA molecules whose functionality, maturation, and regulation requires formation of correct secondary structure and RNA-protein interactions. However, the global influence of these features on plant gene expression is still largely unclear. We have recently developed a high-throughput sequencing based approach that allows a simultaneous view of

the RNA secondary structure and RNA-protein interaction site landscapes transcriptome-wide in eukaryotes. We have used this approach on multiple plant species and during their responses to various conditions and treatments. Our most recent findings in the context of plant salt stress response, where we have found a dramatic shift in RNA secondary structure that correlates with ribosome dynamics of specific sets of transcripts, will be discussed.

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